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Batch Blast Extractor: an automated blastx parser application

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Abstract

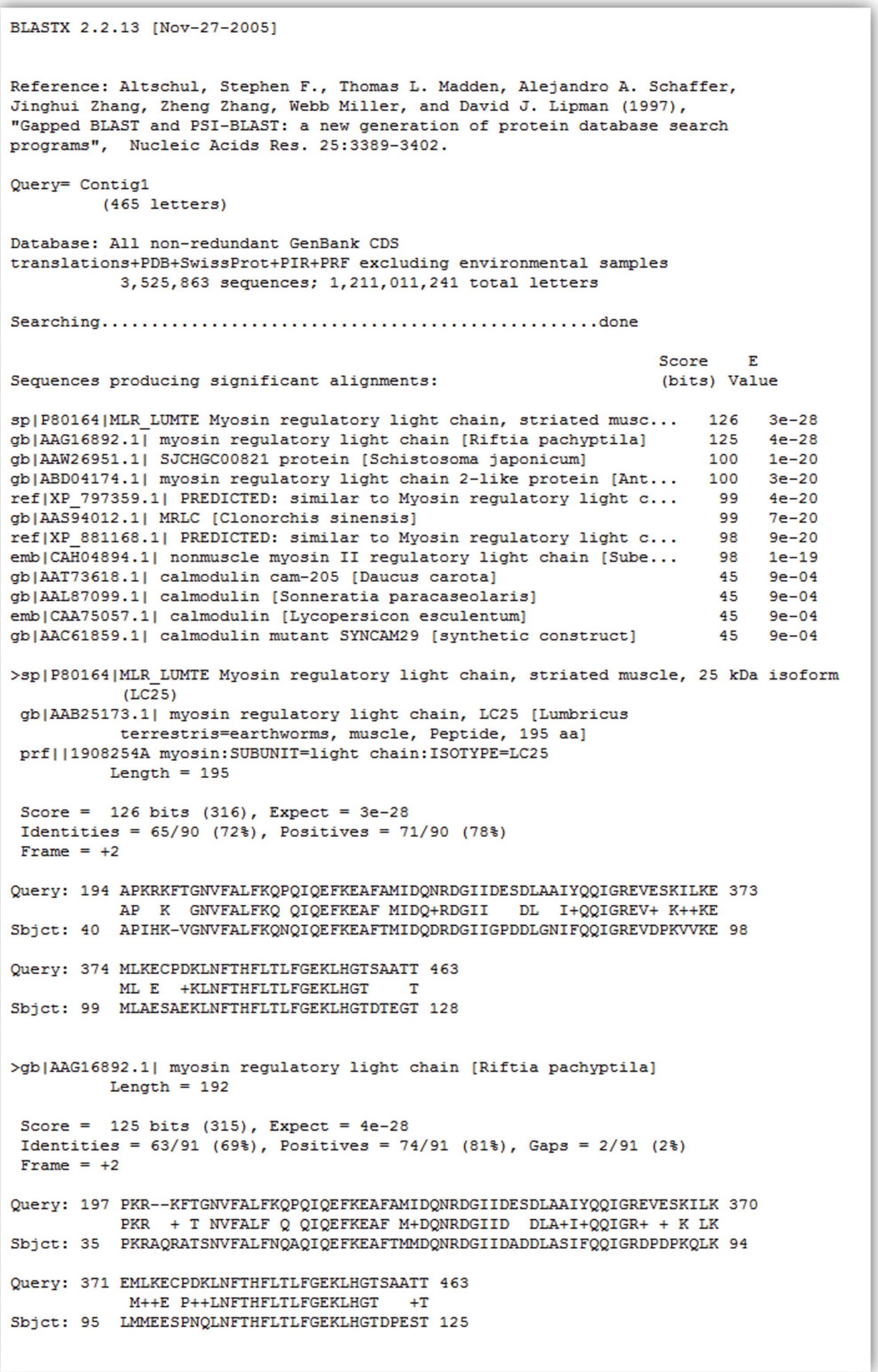
Motivation: BLAST programs are very efficient in finding similarities for sequences. However for large datasets such as ESTs, manual extraction of the information from the batch BLAST output is needed. This can be time consuming, insufficient, and inaccurate. Therefore implementation of a parser application would be extremely useful in extracting information from BLAST outputs.

Results: We have developed a java application, Batch Blast Extractor, with a user friendly graphical interface to extract information from BLAST output. The application generates a tab delimited text file that can be easily imported into any statistical package such as Excel or SPSS for further analysis. For each BLAST hit, the program obtains and saves the essential features from the BLAST output file that would allow further analysis. The program was written in Java and therefore is OS independent. It works on both Windows and Linux OS with java 1.4 and higher. It is freely available from: http://mcbc.usm.edu/BatchBlastExtractor/

Background

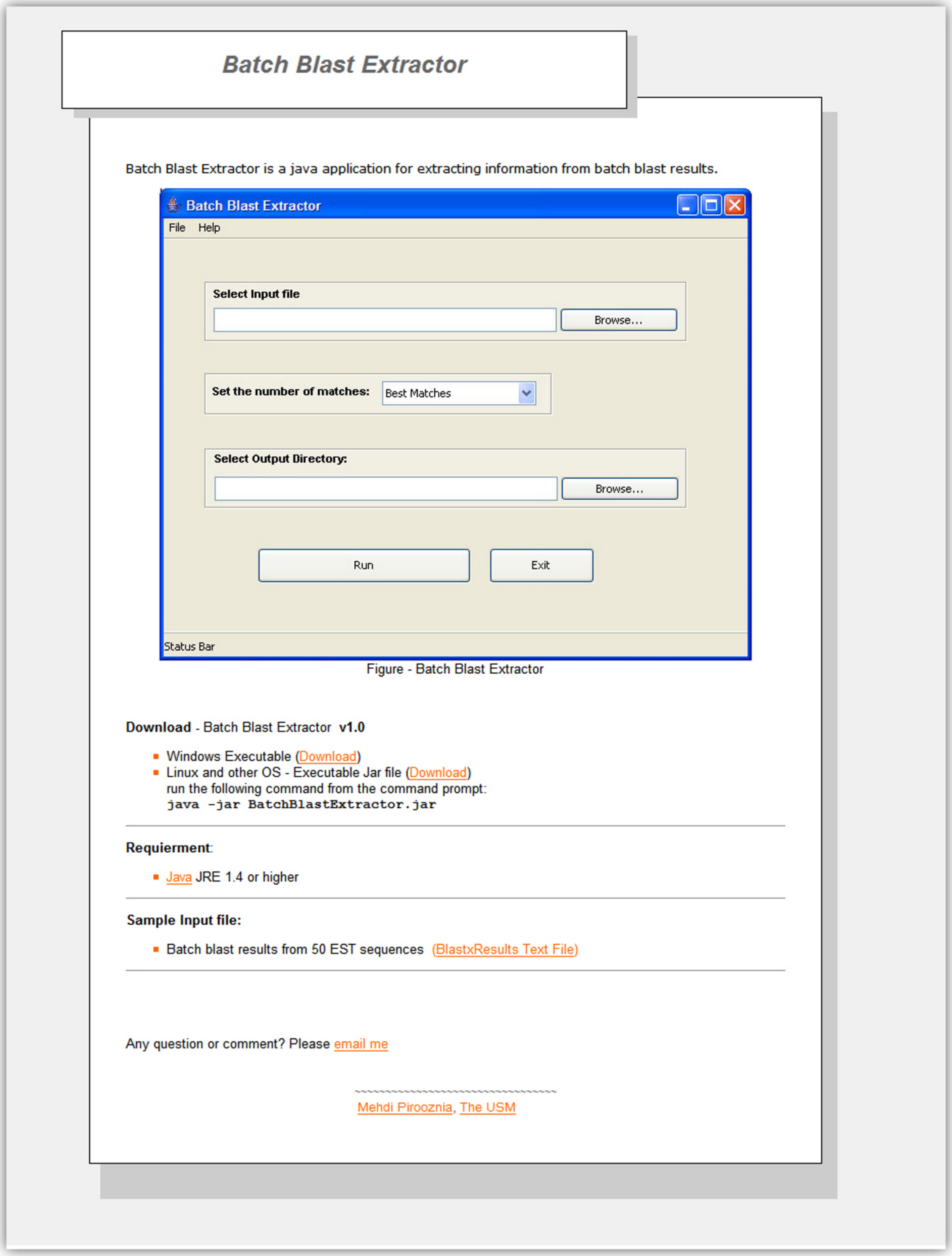
The NCBI BLAST database search tool is one of the most popular programs designed to solve single query problems. BLAST (Basic Local Alignment Search Tool) is the heuristic search algorithm employed by the programs blastp, blastn, blastx, tblastn, and tblastx. The BLAST programs were tailored for sequence similarity searching for example to identify homologs of a given query sequence [1].

The five common BLAST programs perform the following tasks: 1) blastp compares an amino acid query sequence against a protein sequence database; 2) blastn compares a nucleotide query sequence against a nucleotide sequence database; 3) blastx compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database 4) tblastn compares a protein query sequence against a nucleotide sequence database dynamically translated in all six reading frames (both strands), and 5) tblastx compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.



```
BLASTX 2.2.13 [Nov-27-2005]


Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs",  Nucleic Acids Res. 25:3389-3402.

Query= Contig1
         (465 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
           3,525,863 sequences; 1,211,011,241 total letters

Searching.................................................done

                                                                 Score    E
Sequences producing significant alignments:                      (bits) Value

sp|P80164|MLR_LUMTE Myosin regulatory light chain, striated musc...   126   3e-28
gb|AAG16892.1| myosin regulatory light chain [Riftia pachyptila]      125   4e-28
gb|AAW26951.1| SJCHGC00821 protein [Schistosoma japonicum]            100   1e-20
gb|ABD04174.1| myosin regulatory light chain 2-like protein [Ant...   100   3e-20
ref|XP_797359.1| PREDICTED: similar to Myosin regulatory light c...    99   4e-20
gb|AAS94012.1| MRLC [Clonorchis sinensis]                              99   7e-20
ref|XP_881168.1| PREDICTED: similar to Myosin regulatory light c...    98   9e-20
emb|CAH04894.1| nonmuscle myosin II regulatory light chain [Sube...    98   1e-19
gb|AAT73618.1| calmodulin cam-205 [Daucus carota]                      45   9e-04
gb|AAL87099.1| calmodulin [Sonneratia paracaseolaris]                  45   9e-04
emb|CAA75057.1| calmodulin [Lycopersicon esculentum]                   45   9e-04
gb|AAC61859.1| calmodulin mutant SYNCAM29 [synthetic construct]        45   9e-04

>sp|P80164|MLR_LUMTE Myosin regulatory light chain, striated muscle, 25 kDa isoform
           (LC25)
 gb|AAB25173.1| myosin regulatory light chain, LC25 [Lumbricus
           terrestris=earthworms, muscle, Peptide, 195 aa]
 prf||1908254A myosin:SUBUNIT=light chain:ISOTYPE=LC25
          Length = 195

 Score =  126 bits (316), Expect = 3e-28
 Identities = 65/90 (72%), Positives = 71/90 (78%)
 Frame = +2

Query: 194 APKRKFTGNVFALFKQPQIQEFKEAFAMIDQNRDGIIDESDLAAIYQQIGREVESKILKE 373
           AP  K  GNVFALFKQ QIQEFKEAF MIDQ+RDGII   DL  I+QQIGREV+ K++KE
Sbjct: 40  APIHK-VGNVFALFKQNQIQEFKEAFTMIDQDRDGIIGPDDLGNIFQQIGREVDPKVVKE 98

Query: 374 MLKECPDKLNFTHFLTLFGEKLHGTSAATT 463
           ML E  +KLNFTHFLTLFGEKLHGT    T
Sbjct: 99  MLAESAEKLNFTHFLTLFGEKLHGTDTEGT 128


>gb|AAG16892.1| myosin regulatory light chain [Riftia pachyptila]
          Length = 192

 Score =  125 bits (315), Expect = 4e-28
 Identities = 63/91 (69%), Positives = 74/91 (81%), Gaps = 2/91 (2%)
 Frame = +2

Query: 197 PKR--KFTGNVFALFKQPQIQEFKEAFAMIDQNRDGIIDESDLAAIYQQIGREVESKILK 370
           PKR  + T NVFALF Q QIQEFKEAF M+DQNRDGIID  DLA+I+QQIGR+ + K LK
Sbjct: 35  PKRAQRATSNVFALFNQAQIQEFKEAFTMMDQNRDGIIDADDLASIFQQIGRDPDPKQLK 94

Query: 371 EMLKECPDKLNFTHFLTLFGEKLHGTSAATT 463
            M++E P++LNFTHFLTLFGEKLHGT   +T
Sbjct: 95  LMMEESPNQLNFTHFLTLFGEKLHGTDPEST 125
```

Figure 1
Screenshot of a Blastx Output.



Batch Blast Extractor

Batch Blast Extractor is a java application for extracting information from batch blast results.

Figure - Batch Blast Extractor

Download - Batch Blast Extractor **v1.0**

- Windows Executable (Download)
- Linux and other OS - Executable Jar file (Download)
  run the following command from the command prompt:

```
java -jar BatchBlastExtractor.jar
```

Requierment:

- Java JRE 1.4 or higher

Sample Input file:

- Batch blast results from 50 EST sequences (BlastxResults Text File)

Any question or comment? Please email me

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Mehdi Pirooznia, The USM

Figure 2
Screenshot of the Batch Blast Extractor Web site.
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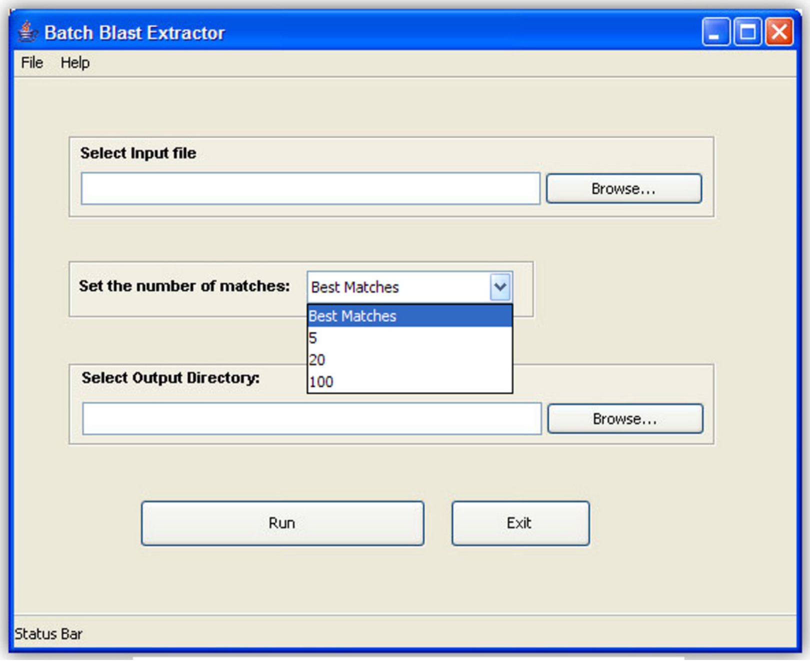

Set the number of matches: Best Matches

Figure 3
The Bach Blast Extractor Graphical User Interface.

The BLAST programs all provide information in roughly the same format. First comes (A) an introduction to the program; (B) a histogram of expectations if one was requested; (C) a series of one-line descriptions of matching database sequences; (D) the actual sequence alignments, and finally the parameters and other statistics gathered during the search. However, for genome-wide comparisons involving multiple queries (batch query), the search is a challenge. For instance, EST collections are currently produced for many species as an efficient strategy for gene identification. Analysis of the ESTs involves clustering, contig formation and annotation of thousands of fragments, interpretation of which may involve thousands of individual BLAST searches [2-5]. An automated post processing of the output (Figure 1) can simplify the analysis in such cases. The blast parser (BlastLikeSaxParser) in BioJava [6] and BPlite from BioPerl [7] are frequently being used to parse a variety of different blast outputs, but neither are user friendly and therefore programming skills are needed to use these applications.

We developed the "Batch Blast Extractor" program (Figure 2 and 3) for use in this regard. It serves as a parser storing only the essential features of BLAST hits in a tabular form. The user can then apply a number of selection criteria to filter out hits with particular attributes. "Batch Blast Extractor" thus serves as a powerful annotation tool for large sets of query sequences.

Results

The application generates a tab delimited text file that can be easily imported into any statistical package such as Excel or SPSS for further analysis. For each BLAST hit, the program derives and saves the following features: Query ID, Query Length, Accession version and GI number, Alignment Length, Score, bit, E-value, Identities, Positives, Gaps, Frame, Organism, and Description.

The extracted information includes the following:

- Query: headers of sequences to analyze

- Subject: headers of sequences found in the database

- Score: a number representation (e.g. 550)

- Score Text: full text representation plus BITS (e.g. 235 bits (450))

- Expect: the E-Value as number (e.g. 1e-166)

- Identities %: a number representation (e.g. 85)

- Identities Text: full text representation plus characters matching (e.g. 110/130 (90%))

- Positives %: a number representation (e.g. 92)

- Positives Text: full text representation (e.g. 110/130 (90%))

- Gaps %: a number representation (e.g. 11)

- Gaps Text: full text representation plus voids (e.g. 9/102 (9%))

- Frame: orientation of the translated ORF (e.g. +3)

- Length Query: the number of nucleotides or amino acids (e.g. 400)

- Length Subject: the number of nucleotides or amino acids (e.g. 500)

- Position Query: as text representation plus the length of the frame (e.g. 328–600 (360))

- Position Subject: as text representation plus the length of the frame (e.g. 1–110 (120))

The program was written in Java. It is OS independent and works on both Windows and Linux OS with java 1.4 and higher. It is freely available to noncommercial users from: http://mcbc.usm.edu/BatchBlastExtractor/ (Figure 2 and 3).

Currently the application works with blastx results. Efforts to extend functionality to other BLAST programs such as blastp and blastn are in progress.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

MP and YD initiated the project. MP designed, programmed and implemented the application and drafted the manuscript. EJP and YP directed the project. All authors read and approved the final manuscript.

Acknowledgements

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References

1. Altschul SF, Madden TL, Schaffer AA, Zhang J, Zhang Z, Miller W, Lipman DJ: **Gapped BLAST and PSI-BLAST: a new generation of protein database search programs.** *Nucleic Acids Res* 1997, **25(17):**3389-3402.
2. Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS, Eppig JT, *et al.*: **Gene ontology: tool for the unification of biology. The Gene Ontology Consortium.** *Nat Genet* 2000, **25(1):**25-29.
3. Liang C, Wang G, Liu L, Ji G, Liu Y, Chen J, Webb JS, Reese G, Dean JF: **WebTraceMiner: a web service for processing and mining EST sequence trace files.** *Nucleic Acids Res* 2007:W137-142.
4. Nagaraj SH, Deshpande N, Gasser RB, Ranganathan S: **ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform.** *Nucleic Acids Res* 2007:W143-147.
5. Pirooznia M, Gong P, Guan X, Inouye LS, Yang K, Perkins EJ, Deng Y: **Cloning, analysis and functional annotation of expressed sequence tags from the Earthworm Eisenia fetida.** *BMC Bioinformatics* 2007, **8(Suppl 7):**S7.
6. Mangalam H: **The Bio* toolkits – a brief overview.** *Brief Bioinform* 2002, **3(3):**296-302.
7. Stajich JE, Block D, Boulez K, Brenner SE, Chervitz SA, Dagdigian C, Fuellen G, Gilbert JG, Korf I, Lapp H, *et al.*: **The Bioperl toolkit: Perl modules for the life sciences.** *Genome Res* 2002, **12(10):**1611-1618.